DT05 Rec'd PCT/PTO 2 1 OCT 2004

WO 03/089932

SEQUENCE LISTING

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ttc ct Phe Le tct cg Ser Ar cag gt Gln Va 40 gtg ca Val H	ac acc ctg tu Thr Leu 10 gg att gtg rg Ile Val 25 rg ctt gtg al Leu Val	tcc Ser gga Gly gcc Ala tgg Trp	gtg Val ggc Gly tct ser gtc Val 60	acg Thr tgg Trp cgt Arg 45 ctc Leu	tgg Trp gag Glu 30 ggc Gly aca Thr	att Ile 15 tgc Cys agg Arg gct Ala	ggt Gly gag Glu gca Ala gcc Ala	Met 1 gct Ala aag Lys gtc Val cac His 65	gca Ala cat His tgc Cys 50 tgc Cys	ccc Pro tcc Ser 35 ggc Gly atc	ctc Leu 20 caa Gln ggt Gly agg Arg	atc Ile ccc Pro gtt Val aac Asn gac	tgg Trp ctg Leu aaa Lys 70		103 151 199
ttc ct Phe Le tct cg Ser Ar cag gt Gln Va 40 gtg ca Val Hi 55 agc gt Ser Va	acc ctg tu Thr Leu 10 gg att gtg gg Ile Val 25 gg ctt gtg al Leu Val ac ccc cag is Pro Gln	tcc Ser gga Gly gcc Ala tgg Trp ctg Leu 75	gtg Val ggc Gly tct Ser gtc Val 60 ggt Gly	acg Thr tgg Trp cgt Arg 45 ctc Leu cgg Arg	tgg Trp gag Glu 30 ggc Gly aca Thr	att Ile 15 tgc Cys agg Arg gct Ala agc Ser	ggt Gly gag Glu gca Ala gcc Ala ctg Leu 80	Met 1 gct Ala aag Lys gtc Val cac His 65 ttt Phe cca	gca Ala cat His tgc Cys 50 tgc Cys cat His	ccc Pro tcc Ser 35 ggc Gly atc Ile	ctc Leu 20 caa Gln ggt Gly agg Arg	atc Ile ccc Pro gtt Val aac Asn gac Asp 85 tac	tgg Trp ctg Leu aaa Lys 70 aca Thr		103 151 199 247

110

105

115

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cac gac cto His Asp Lev 120	atg ctg Met Leu	ctc cgc ct Leu Arg Le 125	g tca gag u Ser Glu	cct gcc gag cto Pro Ala Glu Leo 130	e acg gat I Thr Asp	439
gct gtg aag Ala Val Lys 135	Val Met	gac ctg cc Asp Leu Pr 140	o Thr Gln	gag cca gca cto Glu Pro Ala Leo 145	g ggg acc 1 Gly Thr 150	487
acc tgc tac Thr Cys Tyr	gcc tca Ala Ser 155	ggc tgg gg Gly Trp Gl	c agc att y Ser Ile 160	gaa cca gag gag Glu Pro Glu Glu	g tgt acg 1 Cys Thr 165	535
cct ggg cca Pro Gly Pro	a gat ggt o Asp Gly 170	gca gcc gg Ala Ala Gl	g agc cca y Ser Pro 175	gat gcc tgg gto Asp Ala Trp Val 180	L	577
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gtgtggacct	ccatgttat	t tccaatga	.cg tgtgtgc	gca agttcaccct	cagaaggtga	757
ccaagttcat	gctgtgtgc	t ggacgctg	ga caggggg	caa aagcacctgc	tcgggtgatt	817
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				ıctg agagagtgga		1297
				gga ggcacaacgc		1357
				tcc tggaggcact	•	1417
				.ggc atgggatggg		1477
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<211> 180

<212> PRT

<213> Human

<400> 2

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Ala Ala Pro Leu Ile Leu Ser Arg Ile Val Gly Gly Trp Glu Cys Glu 20 25

Lys His Ser Gln Pro Trp Gln Val Leu Val Ala Ser Arg Gly Arg Ala

Val Cys Gly Gly Val Leu Val His Pro Gln Trp Val Leu Thr Ala Ala 55

His Cys Ile Arg Asn Lys Ser Val Ile Leu Leu Gly Arg His Ser Leu 70

Phe His Pro Glu Asp Thr Gly Gln Val Phe Gln Val Ser His Ser Phe 85

Pro His Pro Leu Tyr Asp Met Ser Leu Leu Lys Asn Arg Phe Leu Arg 105 100

Pro Gly Asp Asp Ser Ser His Asp Leu Met Leu Leu Arg Leu Ser Glu 115 120

Pro Ala Glu Leu Thr Asp Ala Val Lys Val Met Asp Leu Pro Thr Gln 130 135

Glu Pro Ala Leu Gly Thr Thr Cys Tyr Ala Ser Gly Trp Gly Ser Ile 150 155 145

Glu Pro Glu Glu Cys Thr Pro Gly Pro Asp Gly Ala Ala Gly Ser Pro

Asp Ala Trp Val 180

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<213> Human

<220>

<221> CDS

<222> (1)..(489)

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cat His	tcc Ser	caa Gln	ccc Pro 20	tgg Trp	cag Gln	gtg Val	ctt Leu	gtg Val 25	gcc Ala	tct Ser	cgt Arg	ggc Gly	agg Arg 30	gca Ala	gtc Val		96
tgc Cys	ggc Gly	ggt Gly 35	gtt Val	ctg Leu	gtg Val	cac His	ccc Pro 40	cag Gln	tgg Trp	gtc Val	ctc Leu	aca Thr 45	gct Ala	gcc Ala	cac His	٠	144
					agc Ser												192
cat His 65	cct Pro	gaa Glu	gac Asp	aca Thr	ggc Gly 70	cag Gln	gta Val	ttt Phe	cag Gln	gtc Val 75	agc Ser	cac His	agc Ser	ttc Phe	cca Pro 80		240
					atg Met												288
ggt Gly	gat Asp	gac Asp	tcc Ser 100	agc Ser	cac His	gac Asp	ctc Leu	atg Met 105	ctg Leu	ctc Leu	cgc Arg	ctg Leu	tca Ser 110	gag Glu	cct Pro		336
gcc Ala	gag Glu	ctc Leu 115	acg Thr	gat Asp	gct Ala	gtg Val	aag Lys 120	gtc Val	atg Met	gac Asp	ctg Leu	ccc Pro 125	acc Thr	cag Gln	gag Glu		384
					acc Thr												432
					cct Pro 150												480
_	tgg Trp	_	tga													,	492

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<211> 163

<212> PRT

<213> Human

<400> 4

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1 10 15

His Ser Gln Pro Trp Gln Val Leu Val Ala Ser Arg Gly Arg Ala Val

Cys Gly Gly Val Leu Val His Pro Gln Trp Val Leu Thr Ala Ala His 35 40 45

Cys Ile Arg Asn Lys Ser Val Ile Leu Leu Gly Arg His Ser Leu Phe 50 55 His Pro Glu Asp Thr Gly Gln Val Phe Gln Val Ser His Ser Phe Pro 70 His Pro Leu Tyr Asp Met Ser Leu Leu Lys Asn Arg Phe Leu Arg Pro 85 90 Gly Asp Asp Ser Ser His Asp Leu Met Leu Leu Arg Leu Ser Glu Pro 100 Ala Glu Leu Thr Asp Ala Val Lys Val Met Asp Leu Pro Thr Gln Glu 120 Pro Ala Leu Gly Thr Thr Cys Tyr Ala Ser Gly Trp Gly Ser Ile Glu 135 Pro Glu Glu Cys Thr Pro Gly Pro Asp Gly Ala Ala Gly Ser Pro Asp 155 150 Ala Trp Val <210> 5 <211> 471 <212> DNA <213> Human <220> <221> CDS <222> (1)..(468) 48 att gtg gga ggc tgg gag tgc gag aag cat tcc caa ccc tgg cag gtg Ile Val Gly Gly Trp Glu Cys Glu Lys His Ser Gln Pro Trp Gln Val ctt gtg gcc tct cgt ggc agg gca gtc tgc ggc ggt gtt ctg gtg cac 96 Leu Val Ala Ser Arg Gly Arg Ala Val Cys Gly Gly Val Leu Val His 25 ccc cag tgg gtc ctc aca gct gcc cac tgc atc agg aac aaa agc gtg 144 Pro Gln Trp Val Leu Thr Ala Ala His Cys Ile Arg Asn Lys Ser Val 35 40 atc ttg ctg ggt cgg cac agc ctg ttt cat cct gaa gac aca ggc cag 192 Ile Leu Leu Gly Arg His Ser Leu Phe His Pro Glu Asp Thr Gly Gln 60 50 55

gta Val 65	ttt Phe	cag Gln	gtc Val	agc Ser	cac His 70	agc Ser	ttc Phe	cca Pro	cac His	ccg Pro 75	ctc Leu	tac Tyr	gat Asp	atg Met	agc Ser 80	240
ctc Leu	ctg Leu	aag Lys	aat Asn	cga Arg 85	ttc Phe	ctc Leu	agg Arg	cca Pro	ggt Gly 90	gat Asp	gac Asp	tcc Ser	agc Ser	cac His 95	gac Asp	288
ctc Leu	atg Met	ctg Leu	ctc Leu 100	cgc Arg	ctg Leu	tca Ser	gag Glu	cct Pro 105	gcc Ala	gag Glu	ctc Leu	acg Thr	gat Asp 110	gct Ala	gtg Val	336
aag Lys	gtc Val	atg Met 115	gac Asp	ctg Leu	ccc Pro	acc Thr	cag Gln 120	gag Glu	cca Pro	gca Ala	ctg Leu	999 Gly 125	acc Thr	acc Thr	tgc Cys	384
tac Tyr	gcc Ala 130	tca Ser	ggc Gly	tgg Trp	ggc Gly	agc Ser 135	att Ile	gaa Glu	cca Pro	gag Glu	gag Glu 140	tgt Cys	acg Thr	cct Pro	glà aaa	432
				gcc Ala							gtc Val	tga				471
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<400> 6

Ile Val Gly Gly Trp Glu Cys Glu Lys His Ser Gln Pro Trp Gln Val 1 . 5

Leu Val Ala Ser Arg Gly Arg Ala Val Cys Gly Gly Val Leu Val His 25

Pro Gln Trp Val Leu Thr Ala Ala His Cys Ile Arg Asn Lys Ser Val 35

Ile Leu Leu Gly Arg His Ser Leu Phe His Pro Glu Asp Thr Gly Gln 55 50

Val Phe Gln Val Ser His Ser Phe Pro His Pro Leu Tyr Asp Met Ser 70 75

Leu Leu Lys Asn Arg Phe Leu Arg Pro Gly Asp Asp Ser Ser His Asp 90 85

Leu Met Leu Leu Arg Leu Ser Glu Pro Ala Glu Leu Thr Asp Ala Val 100 105

Lys Val Met Asp Leu Pro Thr Gln Glu Pro Ala Leu Gly Thr Thr Cys

115 120 125

Tyr Ala Ser Gly Trp Gly Ser Ile Glu Pro Glu Glu Cys Thr Pro Gly 130 135 140

Pro Asp Gly Ala Ala Gly Ser Pro Asp Ala Trp Val 145 150 155

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<211> 708

<212> DNA

<213> Human

<220>

<221> misc feature

<222> (38)..(577)

<223> CDS

<400> 7

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Cys Thr Pro Gly Pro Asp Gly Ala Ala Gly Ser Pro Asp Ala Trp Val 1 5 10 15

<210> 9 <211> 1541

<210> 8

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<221> CDS

<222> (17)..(685)

<400> 9

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Met Trp Asp Leu Val Leu Ser Ile Ala Leu Ser Val

1 5 10

ggg tgc act ggt gcc gtg ccc ctc atc cag tct cgg att gtg gga ggc 100
Gly Cys Thr Gly Ala Val Pro Leu Ile Gln Ser Arg Ile Val Gly Gly
20 25

tgg gag tgt gag aag cat tcc caa ccc tgg cag gtg gct gtg tac agt

Trp Glu Cys Glu Lys His Ser Gln Pro Trp Gln Val Ala Val Tyr Ser

30 35 40

cat gga tgg gca cac tgt ggg ggt gtc ctg gtg cac ccc cag tgg gtg
His Gly Trp Ala His Cys Gly Gly Val Leu Val His Pro Gln Trp Val
45 50 55 60

ctc aca gct gcc cat tgc cta aag aag aat agc cag gtc tgg ctg ggt
Leu Thr Ala Ala His Cys Leu Lys Lys Asn Ser Gln Val Trp Leu Gly
65 70 75

cgg cac aac ctg ttt gag cct gaa gac aca ggc cag agg gtc cct gtc 292 Arg His Asn Leu Phe Glu Pro Glu Asp Thr Gly Gln Arg Val Pro Val 80 85 90

agc cac agc ttc cca cac ccg ctc tac aat atg agc ctt ctg aag cat

Ser His Ser Phe Pro His Pro Leu Tyr Asn Met Ser Leu Leu Lys His

95 100 105

caa agc ctt aga cca gat gaa gac tcc agc cat gac ctc atg ctg ctc

Gln Ser Leu Arg Pro Asp Glu Asp Ser Ser His Asp Leu Met Leu Leu

110 115 120

436

cgc ctg tca gag cct gcc aag atc aca gat gtt gtg aag gtc ctg ggc Arg Leu Ser Glu Pro Ala Lys Ile Thr Asp Val Val Lys Val Leu Gly 125 130 135 140

ctg ccc acc cag gag cca gca ctg ggg acc acc tgc tac gcc tca ggc
Leu Pro Thr Gln Glu Pro Ala Leu Gly Thr Thr Cys Tyr Ala Ser Gly
145
150
155

tgg ggc agc atc gaa cca gag gag ttc ttg cgc ccc agg agt ctt cag
Trp Gly Ser Ile Glu Pro Glu Glu Phe Leu Arg Pro Arg Ser Leu Gln
160 165 170

tgt gtg agc ctc cat ctc ctg tcc aat gac atg tgt gct aga gct tac

Cys Val Ser Leu His Leu Leu Ser Asn Asp Met Cys Ala Arg Ala Tyr

175

180

580

tct gag aag gtg aca gag ttc atg ttg tgt gct ggg ctc tgg aca ggt
Ser Glu Lys Val Thr Glu Phe Met Leu Cys Ala Gly Leu Trp Thr Gly
190 . 195 200

ggt aaa gac act tgt ggg gtg agt cat ccc tac tcc caa cat ctg gag Gly Lys Asp Thr Cys Gly Val Ser His Pro Tyr Ser Gln His Leu Glu 205 210 215 220	676
ggg aaa ggg tgattctggg ggtccacttg tctgtaatgg tgtgcttcaa Gly Lys Gly	725
ggtatcacat catggggccc tgagccatgt gccctgcctg aaaagcctgc tgtgtacacc	785
aaggtggtgc attaccggaa gtggatcaag gacaccatcg cagccaaccc ctgagtgccc	845
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<211> 223 <212> PRT <213> Human

<400> 10

Met Trp Asp Leu Val Leu Ser Ile Ala Leu Ser Val Gly Cys Thr Gly

Ala Val Pro Leu Ile Gln Ser Arg Ile Val Gly Gly Trp Glu Cys Glu 25

Lys His Ser Gln Pro Trp Gln Val Ala Val Tyr Ser His Gly Trp Ala 35

His Cys Gly Gly Val Leu Val His Pro Gln Trp Val Leu Thr Ala Ala 50 55 60

His Cys Leu Lys Lys Asn Ser Gln Val Trp Leu Gly Arg His Asn Leu

65 70 75 80

Phe Glu Pro Glu Asp Thr Gly Gln Arg Val Pro Val Ser His Ser Phe 85 90 95

Pro His Pro Leu Tyr Asn Met Ser Leu Leu Lys His Gln Ser Leu Arg 100 105 110

Pro Asp Glu Asp Ser Ser His Asp Leu Met Leu Leu Arg Leu Ser Glu 115 120 125

Pro Ala Lys Ile Thr Asp Val Val Lys Val Leu Gly Leu Pro Thr Gln 130 135 140

Glu Pro Ala Leu Gly Thr Thr Cys Tyr Ala Ser Gly Trp Gly Ser Ile 145 150 155 160

Glu Pro Glu Glu Phe Leu Arg Pro Arg Ser Leu Gln Cys Val Ser Leu 165 170 175

His Leu Leu Ser Asn Asp Met Cys Ala Arg Ala Tyr Ser Glu Lys Val 180 185 190

Thr Glu Phe Met Leu Cys Ala Gly Leu Trp Thr Gly Gly Lys Asp Thr 195 200 205

Cys Gly Val Ser His Pro Tyr Ser Gln His Leu Glu Gly Lys Gly 210 215 220

<210> 11

<211> 621

<212> DNA

<213> Human

<220>

<221> CDS

<222> (1)..(618)

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Val Pro Leu Ile Gln Ser Arg Ile Val Gly Gly Trp Glu Cys Glu Lys
1 10 15

cat tcc caa ccc tgg cag gtg gct gtg tac agt cat gga tgg gca cac 96
His Ser Gln Pro Trp Gln Val Ala Val Tyr Ser His Gly Trp Ala His
20 25 30

tgt ggg ggt gtc ctg gtg cac ccc cag tgg gtg ctc aca gct gcc cat

Cys Gly Val Leu Val His Pro Gln Trp Val Leu Thr Ala Ala His

35 40 45

tgc Cys	cta Leu 50	aag Lys	aag Lys	aat Asn	agc Ser	cag Gln 55	gtc Val	tgg Trp	ctg Leu	ggt Gly	cgg Arg 60	cac His	aac Asn	ctg Leu	ttt Phe	192
gag Glu 65	cct Pro	gaa Glu	gac Asp	aca Thr	ggc Gly 70	cag Gln	agg Arg	gtc Val	.cct Pro	gtc Val 75	agc Ser	cac His	agc Ser	ttc Phe	cca Pro 80	240
cac His	ccg Pro	ctc Leu	tac Tyr	aat Asn 85	atg Met	agc Ser	ctt Leu	ctg Leu	aag Lys 90	cat His	caa Gln	agc Ser	ctt Leu	aga Arg 95	cca Pro	288
									ctg Leu							336
									ctg Leu							384
cca Pro	gca Ala 130	ctg Leu	gly ggg	acc Thr	acc Thr	tgc Cys 135	tac Tyr	gcc Ala	tca Ser	ggc Gly	tgg Trp 140	ggc Gly	agc Ser	atc Ile	gaa Glu	432
cca Pro 145	gag Glu	gag Glu	ttc Phe	ttg Leu	cgc Arg 150	ccc Pro	agg Arg	agt Ser	ctt Leu	cag Gln 155	tgt Cys	gtg Val	agc Ser	ctc Leu	cat His 160	480
ctc Leu	ctg Leu	tcc Ser	aat Asn	gac Asp 165	atg Met	tgt Cys	gct Ala	aga Arg	gct Ala 170	tac Tyr	tct Ser	gag Glu	aag Lys	gtg Val 175	aca Thr	528
									aca Thr							576
									ctg Leu					tga		621
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<210> 12

<211> 206

<212> PRT

<213> Human

<400> 12

Val Pro Leu Ile Gln Ser Arg Ile Val Gly Gly Trp Glu Cys Glu Lys
1 5 10 15

His Ser Gln Pro Trp Gln Val Ala Val Tyr Ser His Gly Trp Ala His 20 25 30

Cys Gly Gly Val Leu Val His Pro Gln Trp Val Leu Thr Ala Ala His 35 40 45

Cys Leu Lys Lys Asn Ser Gln Val Trp Leu Gly Arg His Asn Leu Phe 50 55 60

Glu Pro Glu Asp Thr Gly Gln Arg Val Pro Val Ser His Ser Phe Pro 65 70 75 80

His Pro Leu Tyr Asn Met Ser Leu Leu Lys His Gln Ser Leu Arg Pro 85 90 95

Asp Glu Asp Ser Ser His Asp Leu Met Leu Leu Arg Leu Ser Glu Pro 100 105 110

Ala Lys Ile Thr Asp Val Val Lys Val Leu Gly Leu Pro Thr Gln Glu 115 120 125

Pro Ala Leu Gly Thr Thr Cys Tyr Ala Ser Gly Trp Gly Ser Ile Glu 130 135 140

Pro Glu Glu Phe Leu Arg Pro Arg Ser Leu Gln Cys Val Ser Leu His 145 150 155 160

Leu Leu Ser Asn Asp Met Cys Ala Arg Ala Tyr Ser Glu Lys Val Thr 165 170 175

Glu Phe Met Leu Cys Ala Gly Leu Trp Thr Gly Gly Lys Asp Thr Cys 180 185 190

Gly Val Ser His Pro Tyr Ser Gln His Leu Glu Gly Lys Gly 195 200 205

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<211> 600

<212> DNA

<213> Human

<220>

<221> CDS

<222> (1)..(597)

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1 5 10 15

96

gct gtg tac agt cat gga tgg gca cac tgt ggg ggt gtc ctg gtg cac Ala Val Tyr Ser His Gly Trp Ala His Cys Gly Gly Val Leu Val His 20 25 30

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Pro Gln Trp Val Leu Thr Ala Ala His Cys Leu Lys Lys Asn Ser Gln

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Val Trp Leu Gly Arg His Asn Leu Phe Glu Pro Glu Asp Thr Gly Gln 50 55 60

Arg Val Pro Val Ser His Ser Phe Pro His Pro Leu Tyr Asn Met Ser 65 70 75 80

Leu Leu Lys His Gln Ser Leu Arg Pro Asp Glu Asp Ser Ser His Asp 85 90 95

Leu Met Leu Leu Arg Leu Ser Glu Pro Ala Lys Ile Thr Asp Val Val 100 105 110

Lys Val Leu Gly Leu Pro Thr Gln Glu Pro Ala Leu Gly Thr Thr Cys 115 120 125

Tyr Ala Ser Gly Trp Gly Ser Ile Glu Pro Glu Glu Phe Leu Arg Pro 130 135 140

Arg Ser Leu Gln Cys Val Ser Leu His Leu Leu Ser Asn Asp Met Cys 145 150 155 160

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